

1600

RAW SEQUENCE LISTING

DATE: 11/07/2001

PATENT APPLICATION: US/09/646,224A

TIME: 13:12:37

Input Set : A:\amended.txt

Output Set: N:\CRF3\11072001\I646224A.raw

ENTERED

4 <110> APPLICANT: Glaxo Wellcome PLC
 5 Tate, Simon N
 6 Grose, David T
 7 Hicks, Caroline A
 9 <120> TITLE OF INVENTION: Ion Channels
 11 <130> FILE REFERENCE: PG3432
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/646,224A
 C--> 14 <141> CURRENT FILING DATE: 2000-09-14
 16 <150> PRIOR APPLICATION NUMBER: GB 9805793.8
 17 <151> PRIOR FILING DATE: 1998-03-18
 19 <160> NUMBER OF SEQ ID NOS: 35
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 5897
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Rattus norvegicus
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (49)..(5346)
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 34 Met Glu Glu
 35 1
 37 agg tac tac ccg gtg atc ttc ccg gac gag cgg aat ttc cgc ccc ttc 105
 38 Arg Tyr Tyr Pro Val Ile Phe Pro Asp Glu Arg Asn Phe Arg Pro Phe
 39 5 10 15
 41 act tcc gac tct ctg gct gcc ata aag aag cgg att gct atc caa aag 153
 42 Thr Ser Asp Ser Leu Ala Ala Ile Lys Lys Arg Ile Ala Ile Gln Lys
 43 20 25 30 35
 45 gag agg aag aag tcc aaa gac aag gcg gca gct gag ccc cag cct cgg 201
 46 Glu Arg Lys Lys Ser Lys Asp Lys Ala Ala Ala Glu Pro Gln Pro Arg
 47 40 45 50
 49 cct cag ctt gac cta aag gcc tcc agg aag tta cct aag ctt tat ggt 249
 50 Pro Gln Leu Asp Leu Lys Ala Ser Arg Lys Leu Pro Lys Leu Tyr Gly
 51 55 60 65
 53 gac att ccc cct gag ctt gtt acg aaa cct ctg gag gac ctg gac ccc 297
 54 Asp Ile Pro Pro Glu Leu Val Thr Lys Pro Leu Glu Asp Leu Asp Pro
 55 70 75 80
 57 tac tac aaa gac cat aag aca ttc atg gtg ttg aac aag aaa aga aca 345
 58 Tyr Tyr Lys Asp His Lys Thr Phe Met Val Leu Asn Lys Lys Arg Thr
 59 85 90 95
 61 att tat cgc ttc agc gcc aag cgg gcc ttg ttc att ctg ggg cct ttt 393
 62 Ile Tyr Arg Phe Ser Ala Lys Arg Ala Leu Phe Ile Leu Gly Pro Phe
 63 100 105 110 115
 65 aat ccc ctc aga agc tta atg att cgt atc tct gtc cat tca gtc ttt 441
 66 Asn Pro Leu Arg Ser Leu Met Ile Arg Ile Ser Val His Ser Val Phe
 67 120 125 130

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69	agc atg ttc atc atc tgc acg gtg atc atc aac tgt atg ttc atg gcg	489
70	Ser Met Phe Ile Ile Cys Thr Val Ile Ile Asn Cys Met Phe Met Ala	
71	135 140 145	
73	aat tct atg gag aga agt ttc gac aac gac att ccc gaa tac gtc ttc	537
74	Asn Ser Met Glu Arg Ser Phe Asp Asn Asp Ile Pro Glu Tyr Val Phe	
75	150 155 160	
77	att ggg att tat att tta gaa gct gtg att aaa ata ttg gca aga ggc	585
78	Ile Gly Ile Tyr Ile Leu Glu Ala Val Ile Lys Ile Leu Ala Arg Gly	
79	165 170 175	
81	ttc att gtg gat gag ttt tcc ttc ctc cga gat ccg tgg aac tgg ctg	633
82	Phe Ile Val Asp Glu Phe Ser Phe Leu Arg Asp Pro Trp Asn Trp Leu	
83	180 185 190 195	
85	gac ttc att gtc att gga aca gcg atc gca act tgt ttt ccg ggc agc	681
86	Asp Phe Ile Val Ile Gly Thr Ala Ile Ala Thr Cys Phe Pro Gly Ser	
87	200 205 210	
89	caa gtc aat ctt tca gct ctt cgt acc ttc cga gtg ttc aga gct ctg	729
90	Gln Val Asn Leu Ser Ala Leu Arg Thr Phe Arg Val Phe Arg Ala Leu	
91	215 220 225	
93	aag gcg att tca gtt atc tca ggt ctg aag gtc atc gta ggt gcc ctg	777
94	Lys Ala Ile Ser Val Ile Ser Gly Leu Lys Val Ile Val Gly Ala Leu	
95	230 235 240	
97	ctg cgc tcg gtg aag aag ctg gta gac gtg atg gtc ctc act ctc ttc	825
98	Leu Arg Ser Val Lys Lys Leu Val Asp Val Met Val Leu Thr Leu Phe	
99	245 250 255	
101	tgc ctc agc atc ttt gcc ctg gtc ggt cag cag ctg ttc atg gga att	873
102	Cys Leu Ser Ile Phe Ala Leu Val Gly Gln Gln Leu Phe Met Gly Ile	
103	260 265 270 275	
105	ctg aac cag aag tgt att aag cac aac tgt ggc ccc aac cct gca tcc	921
106	Leu Asn Gln Lys Cys Ile Lys His Asn Cys Gly Pro Asn Pro Ala Ser	
107	280 285 290	
109	aac aag gat tgc ttt gaa aag gaa aaa gat agc gaa gac ttc ata atg	969
110	Asn Lys Asp Cys Phe Glu Lys Glu Lys Asp Ser Glu Asp Phe Ile Met	
111	295 300 305	
113	tgt ggt acc tgg ctc ggc agc aga ccc tgt ccc aat ggt tct acg tgc	1017
114	Cys Gly Thr Trp Leu Gly Ser Arg Pro Cys Pro Asn Gly Ser Thr Cys	
115	310 315 320	
117	gat aaa acc aca ttg aac cca gac aat aat tat aca aag ttt gac aac	1065
118	Asp Lys Thr Thr Leu Asn Pro Asp Asn Asn Tyr Thr Lys Phe Asp Asn	
119	325 330 335	
121	ttt ggc tgg tcc ttt ctc gcc atg ttc cgg gtt atg act caa gac tcc	1113
122	Phe Gly Trp Ser Phe Leu Ala Met Phe Arg Val Met Thr Gln Asp Ser	
123	340 345 350 355	
125	tgg gag agg ctt tac cga cag atc ctg cgg acc tct ggg atc tac ttt	1161
126	Trp Glu Arg Leu Tyr Arg Gln Ile Leu Arg Thr Ser Gly Ile Tyr Phe	
127	360 365 370	
129	gtc ttc ttc ttc gtg gtg gtc atc ttc ctg ggc tcc ttc tac ctg ctt	1209
130	Val Phe Phe Phe Val Val Val Ile Phe Leu Gly Ser Phe Tyr Leu Leu	
131	375 380 385	
133	aac cta acc ctg gct gtt gtc acc atg gct tat gaa gaa cag aac aga	1257

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135				390				395					400				
137	aat	gta	gct	gct	gag	aca	gag	gcc	aag	gag	aaa	atg	ttt	cag	gaa	gcc	1305
138	Asn	Val	Ala	Ala	Glu	Thr	Glu	Ala	Lys	Glu	Lys	Met	Phe	Gln	Glu	Ala	
139		405					410					415					
141	cag	cag	ctg	tta	agg	gag	gag	aag	gag	gct	ctg	gtt	gcc	atg	gga	att	1353
142	Gln	Gln	Leu	Leu	Arg	Glu	Glu	Lys	Glu	Ala	Leu	Val	Ala	Met	Gly	Ile	
143	420					425				430						435	
145	gac	aga	agt	tcc	ctt	aat	tcc	ctt	caa	gct	tca	tcc	ttt	tcc	ccg	aag	1401
146	Asp	Arg	Ser	Ser	Leu	Asn	Ser	Leu	Gln	Ala	Ser	Ser	Phe	Ser	Pro	Lys	
147				440					445						450		
149	aag	agg	aag	ttt	ttc	ggg	agt	aag	aca	aga	aag	tcc	ttc	ttt	atg	aga	1449
150	Lys	Arg	Lys	Phe	Phe	Gly	Ser	Lys	Thr	Arg	Lys	Ser	Phe	Phe	Met	Arg	
151				455					460						465		
153	ggg	tcc	aag	acg	gcc	caa	gcc	tca	gcg	tct	gat	tca	gag	gac	gat	gcc	1497
154	Gly	Ser	Lys	Thr	Ala	Gln	Ala	Ser	Ala	Ser	Asp	Ser	Glu	Asp	Asp	Ala	
155		470					475					480					
157	tct	aaa	aat	cca	cag	ctc	ctt	gag	cag	acc	aaa	cga	ctg	tcc	cag	aac	1545
158	Ser	Lys	Asn	Pro	Gln	Leu	Leu	Glu	Gln	Thr	Lys	Arg	Leu	Ser	Gln	Asn	
159		485					490					495					
161	ttg	cca	gtg	gat	ctc	ttt	gat	gag	cac	gtg	gac	ccc	ctc	cac	agg	cag	1593
162	Leu	Pro	Val	Asp	Leu	Phe	Asp	Glu	His	Val	Asp	Pro	Leu	His	Arg	Gln	
163	500					505				510					515		
165	aga	gcg	ctg	agc	gct	gtc	agt	atc	tta	acc	atc	acc	ata	cag	gaa	caa	1641
166	Arg	Ala	Leu	Ser	Ala	Val	Ser	Ile	Leu	Thr	Ile	Thr	Ile	Gln	Glu	Gln	
167				520				525							530		
169	gaa	aaa	ttc	cag	gag	cct	tgt	ttc	cca	tgt	ggg	aaa	aat	ttg	gcc	tct	1689
170	Glu	Lys	Phe	Gln	Glu	Pro	Cys	Phe	Pro	Cys	Gly	Lys	Asn	Leu	Ala	Ser	
171			535					540					545				
173	aag	tac	ctg	gtg	tgg	gac	tgt	agc	cct	cag	tgg	ctg	tgc	ata	aag	aag	1737
174	Lys	Tyr	Leu	Val	Trp	Asp	Cys	Ser	Pro	Gln	Trp	Leu	Cys	Ile	Lys	Lys	
175		550						555					560				
177	gtc	ctg	cgg	acc	atc	atg	acg	gat	ccc	ttt	act	gag	ctg	gcc	atc	acc	1785
178	Val	Leu	Arg	Thr	Ile	Met	Thr	Asp	Pro	Phe	Thr	Glu	Leu	Ala	Ile	Thr	
179		565					570					575					
181	atc	tgc	atc	atc	atc	aat	acc	gtt	ttc	tta	gcc	gtg	gag	cac	cac	aac	1833
182	Ile	Cys	Ile	Ile	Ile	Asn	Thr	Val	Phe	Leu	Ala	Val	Glu	His	His	Asn	
183	580					585				590					595		
185	atg	gat	gac	aac	tta	aag	acc	ata	ctg	aaa	ata	gga	aac	tgg	gtt	ttc	1881
186	Met	Asp	Asp	Asn	Leu	Lys	Thr	Ile	Leu	Lys	Ile	Gly	Asn	Trp	Val	Phe	
187				600				605							610		
189	acg	gga	att	ttc	ata	gcg	gaa	atg	tgt	ctc	aag	atc	atc	gcg	ctc	gac	1929
190	Thr	Gly	Ile	Phe	Ile	Ala	Glu	Met	Cys	Leu	Lys	Ile	Ile	Ala	Leu	Asp	
191			615					620					625				
193	cct	tac	cac	tac	ttc	cgg	cac	ggc	tgg	aat	gtt	ttt	gac	agc	atc	gtg	1977
194	Pro	Tyr	His	Tyr	Phe	Arg	His	Gly	Trp	Asn	Val	Phe	Asp	Ser	Ile	Val	
195		630						635					640				
197	gcc	ctc	ctg	agt	ctc	gct	gat	gtg	ctc	tac	aac	aca	ctg	tct	gat	aac	2025
198	Ala	Leu	Leu	Ser	Leu	Ala	Asp	Val	Leu	Tyr	Asn	Thr	Leu	Ser	Asp	Asn	

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201 aat agg tct ttc ttg gct tcc ctc aga gtg ctg agg gtc ttc aag tta 2073
202 Asn Arg Ser Phe Leu Ala Ser Leu Arg Val Leu Arg Val Phe Lys Leu
203 660      665      670      675
205 gcc aaa tcc tgg ccc acg tta aac act ctc att aag atc atc ggc cac 2121
206 Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile Ile Gly His
207      680      685      690
209 tcc gtg ggc gcg ctt gga aac ctg act gtg gtc ctg act atc gtg gtc 2169
210 Ser Val Gly Ala Leu Gly Asn Leu Thr Val Val Leu Thr Ile Val Val
211      695      700      705
213 ttc atc ttt tct gtg gtg ggc atg cgg ctc ttc ggc acc aag ttt aac 2217
214 Phe Ile Phe Ser Val Val Gly Met Arg Leu Phe Gly Thr Lys Phe Asn
215      710      715      720
217 aag acc gcc tac gcc acc cag gag cgg ccc agg cgg cgc tgg cac atg 2265
218 Lys Thr Ala Tyr Ala Thr Gln Glu Arg Pro Arg Arg Arg Trp His Met
219      725      730      735
221 gat aat ttc tac cac tcc ttc ctg gtg gtg ttc cgc atc ctc tgt ggg 2313
222 Asp Asn Phe Tyr His Ser Phe Leu Val Val Phe Arg Ile Leu Cys Gly
223 740      745      750      755
225 gaa tgg atc gag aac atg tgg ggc tgc atg cag gat atg gac ggc tcc 2361
226 Glu Trp Ile Glu Asn Met Trp Gly Cys Met Gln Asp Met Asp Gly Ser
227      760      765      770
229 ccg ttg tgc atc att gtc ttt gtc ctg ata atg gtg atc ggg aag ctt 2409
230 Pro Leu Cys Ile Ile Val Phe Val Leu Ile Met Val Ile Gly Lys Leu
231      775      780      785
233 gtg gtg ctt aac ctc ttc att gcc ttg ctg ctc aat tcc ttc agc aat 2457
234 Val Val Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser Phe Ser Asn
235      790      795      800
237 gag gag aag gat ggg agc ctg gaa gga gag acc agg aaa acc aaa gtg 2505
238 Glu Glu Lys Asp Gly Ser Leu Glu Gly Glu Thr Arg Lys Thr Lys Val
239      805      810      815
241 cag cta gcc ctg gat cgg ttc cgc cgg gcc ttc tcc ttc atg ctg cac 2553
242 Gln Leu Ala Leu Asp Arg Phe Arg Arg Ala Phe Ser Phe Met Leu His
243 820      825      830      835
245 gct ctt cag agt ttt tgt tgc aag aaa tgc agg agg aaa aac tcg cca 2601
246 Ala Leu Gln Ser Phe Cys Cys Lys Lys Cys Arg Arg Lys Asn Ser Pro
247      840      845      850
249 aag cca aaa gag aca aca gaa agc ttt gct ggt gag aat aaa gac tca 2649
250 Lys Pro Lys Glu Thr Thr Glu Ser Phe Ala Gly Glu Asn Lys Asp Ser
251      855      860      865
253 atc ctc ccg gat gcg agg ccc tgg aag gag tat gat aca gac atg gct 2697
254 Ile Leu Pro Asp Ala Arg Pro Trp Lys Glu Tyr Asp Thr Asp Met Ala
255      870      875      880
257 ttg tac act gga cag gcc ggg gct ccg ctg gcc cca ctc gca gag gta 2745
258 Leu Tyr Thr Gly Gln Ala Gly Ala Pro Leu Ala Pro Leu Ala Glu Val
259      885      890      895
261 gag gac gat gtg gaa tat tgt ggt gaa ggc ggt gcc cta ccc acc tca 2793
262 Glu Asp Asp Val Glu Tyr Cys Gly Glu Gly Gly Ala Leu Pro Thr Ser
263 900      905      910      915

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266  Gln His Ser Ala Gly Val Gln Ala Gly Asp Leu Pro Pro Glu Thr Lys
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269  cag ctc act agc ccg gat gac caa ggg gtt gaa atg gaa gta ttt tct      2889
270  Gln Leu Thr Ser Pro Asp Asp Gln Gly Val Glu Met Glu Val Phe Ser
271              935                      940                      945
273  gaa gaa gat ctg cat tta agc ata cag agt cct cga aag aag tct gac      2937
274  Glu Glu Asp Leu His Leu Ser Ile Gln Ser Pro Arg Lys Lys Ser Asp
275              950                      955                      960
277  gca gtg agc atg ctc tcg gaa tgc agc aca att gac ctg aat gat atc      2985
278  Ala Val Ser Met Leu Ser Glu Cys Ser Thr Ile Asp Leu Asn Asp Ile
279              965                      970                      975
281  ttt aga aat tta cag aaa aca gtt tcc ccc aaa aag cag cca gat aga      3033
282  Phe Arg Asn Leu Gln Lys Thr Val Ser Pro Lys Lys Gln Pro Asp Arg
283  980                      985                      990                      995
285  tgc ttt ccc aag ggc ctt agt tgt cac ttt cta tgc cac aaa aca gac      3081
286  Cys Phe Pro Lys Gly Leu Ser Cys His Phe Leu Cys His Lys Thr Asp
287              1000                      1005                      1010
289  aag aga aag tcc ccc tgg gtc ctg tgg tgg aac att cgg aaa acc tgc      3129
290  Lys Arg Lys Ser Pro Trp Val Leu Trp Trp Asn Ile Arg Lys Thr Cys
291              1015                      1020                      1025
293  tac caa atc gtg aag cac agc tgg ttt gag agt ttc ata atc ttt gtt      3177
294  Tyr Gln Ile Val Lys His Ser Trp Phe Glu Ser Phe Ile Ile Phe Val
295              1030                      1035                      1040
297  att ctg ctg agc agt gga gcg ctg ata ttt gaa gat gtc aat ctc ccc      3225
298  Ile Leu Leu Ser Ser Gly Ala Leu Ile Phe Glu Asp Val Asn Leu Pro
299              1045                      1050                      1055
301  agc cgg ccc caa gtt gag aaa tta cta agg tgt acc gat aat att ttc      3273
302  Ser Arg Pro Gln Val Glu Lys Leu Leu Arg Cys Thr Asp Asn Ile Phe
303  1060                      1065                      1070                      1075
305  aca ttt att ttc ctc ctg gaa atg atc ctg aag tgg gtg gcc ttt gga      3321
306  Thr Phe Ile Phe Leu Leu Glu Met Ile Leu Lys Trp Val Ala Phe Gly
307              1080                      1085                      1090
309  ttc cgg agg tat ttc acc agt gcc tgg tgc tgg ctt gat ttc ctc att      3369
310  Phe Arg Arg Tyr Phe Thr Ser Ala Trp Cys Trp Leu Asp Phe Leu Ile
311              1095                      1100                      1105
313  gtg gtg gtg tct gtg ctc agt ctc atg aat cta cca agc ttg aag tcc      3417
314  Val Val Val Ser Val Leu Ser Leu Met Asn Leu Pro Ser Leu Lys Ser
315              1110                      1115                      1120
317  ttc cgg act ctg cgg gcc ctg aga cct ctg cgg gcg ctg tcc cag ttt      3465
318  Phe Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser Gln Phe
319              1125                      1130                      1135
321  gaa gga atg aag gtt gtc gtc tac gcc ctg atc agc gcc ata cct gcc      3513
322  Glu Gly Met Lys Val Val Val Tyr Ala Leu Ile Ser Ala Ile Pro Ala
323  1140                      1145                      1150                      1155
325  att ctc aat gtc ttg ctg gtc tgc ctc att ttc tgg ctc gta ttt tgt      3561
326  Ile Leu Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Val Phe Cys
327              1160                      1165                      1170
329  atc ttg gga gta aat tta ttt tct ggg aag ttt gga agg tgc att aac      3609

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L:13 M:270 C: Current Application Number differs, Replaced Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date